

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
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Application Serial Number: 10/589,851  
Source: 1 FWO  
Date Processed by STIC: 1/22/07

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DATE: 01/22/2007

PATENT APPLICATION: US/10/589,851

TIME: 13:08:38

Input Set : E:\MEWB 013 00US SeqList.txt

Output Set: N:\CRF4\01222007\J589851.raw

5 <110> APPLICANT: Trowsdale, John  
6 Eagle, Robert  
7 Bacon, Louise  
11 <120> TITLE OF INVENTION: Protein Ligands for NKG2D and UL16 Receptors and Uses  
Thereof  
15 <130> FILE REFERENCE: MEWB-013/00US  
18 <140> CURRENT APPLICATION NUMBER: US 10/589,851  
20 <141> CURRENT FILING DATE: 2006-08-17  
23 <150> PRIOR APPLICATION NUMBER: PCT/GB2005/000572  
25 <151> PRIOR FILING DATE: 2005-02-17  
29 <150> PRIOR APPLICATION NUMBER: GB 0403491.4  
31 <151> PRIOR FILING DATE: 2004-02-17  
35 <160> NUMBER OF SEQ ID NOS: 16  
39 <170> SOFTWARE: PatentIn version 3.1  
43 <210> SEQ ID NO: 1  
45 <211> LENGTH: 333  
47 <212> TYPE: PRT  
49 <213> ORGANISM: Homo sapiens  
53 <400> SEQUENCE: 1  
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59 Leu Leu Ser Ser Trp Cys Arg Thr Gly Leu Ala Asp Pro His Ser Leu  
60 20 25 30  
63 Cys Tyr Asp Ile Thr Val Ile Pro Lys Ile Arg Pro Gly Pro Arg Trp  
64 35 40 45  
67 Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr Phe Leu His Tyr Asp  
68 50 55 60  
71 Cys Gly Ser Lys Arg Val Thr Pro Val Ser Pro Leu Gly Lys Lys Leu  
72 65 70 75 80  
75 Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro Val Leu Arg Glu Val  
76 85 90 95  
79 Val Asp Ile Leu Thr Glu Gln Leu Leu Asp Ile Gln Leu Glu Asn Tyr  
80 100 105 110  
83 Ile Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg Met Ser Cys Glu Gln  
84 115 120 125  
87 Lys Ala Glu Gly His Gly Ser Gly Ser Trp Gln Pro Ser Phe Asp Gly  
88 130 135 140  
91 Gln Ile Phe Leu Leu Phe Asp Ser Gln Asn Arg Met Trp Thr Thr Thr  
92 145 150 155 160  
95 His Pro Gly Pro Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys Asp  
96 165 170 175  
99 Met Thr Met Ser Phe His Tyr Ile Ser Met Gly Asp Cys Thr Gly Trp  
100 180 185 190  
103 Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser Ala

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108          210          215          220
111 Ala Thr Thr Leu Ile Leu Cys Cys Leu Leu Ile Met Cys Leu Leu Ile
112 225          230          235          240
115 Cys Ser Arg His Ser Leu Thr Gln Ser His Gly His His Pro Gln Ser
116          245          250          255
119 Leu Gln Pro Pro Pro His Pro Pro Leu Leu His Pro Thr Trp Leu Leu
120          260          265          270
123 Arg Arg Val Leu Trp Ser Asp Ser Tyr Gln Ile Ala Lys Arg Pro Leu
124          275          280          285
127 Ser Gly Gly His Val Thr Arg Val Thr Leu Pro Ile Ile Gly Asp Asp
128          290          295          300
131 Ser His Ser Leu Pro Cys Pro Leu Ala Leu Tyr Thr Ile Asn Asn Gly
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143 <212> TYPE: PRT
145 <213> ORGANISM: Homo sapiens
149 <400> SEQUENCE: 2
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155 Leu Leu Ser Ser Trp Cys Arg Thr Gly Leu Ala Asp Pro His Ser Leu
156          20          25          30
159 Cys Tyr Asp Ile Thr Val Ile Pro Lys Ile Arg Pro Gly Pro Arg Trp
160          35          40          45
163 Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr Phe Leu His Tyr Asp
164          50          55          60
167 Cys Gly Ser Lys Arg Val Thr Pro Val Ser Pro Leu Gly Lys Lys Leu
168 65          70          75          80
171 Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro Val Leu Arg Glu Val
172          85          90          95
175 Val Asp Ile Leu Thr Glu Gln Leu Leu Asp Ile Gln Leu Glu Asn Tyr
176          100          105          110
179 Ile Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg Met Ser Cys Glu Gln
180          115          120          125
183 Lys Ala Glu Gly His Gly Ser Gly Ser Trp Gln Pro Ser Phe Asp Gly
184          130          135          140
187 Gln Ile Phe Leu Leu Phe Asp Ser Gln Asn Arg Met Trp Thr Thr Thr
188 145          150          155          160
191 His Pro Gly Pro Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys Asp
192          165          170          175
195 Met Thr Met Ser Phe His Tyr Ile Ser Met Gly Asp Cys Thr Gly Trp
196          180          185          190
199 Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser Ala
200          195          200          205
203 Gly Gly Thr Val

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213 <213> ORGANISM: Homo sapiens
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220 actccccaat ggcagcggcc gccagccccg cgcttccttct acgcctcccg cttctgctcc      120
222 tgctgtccag ctggtgcagg accgggctgg ccgacctca ctctctttgc tatgacatca      180
224 cgtcatccc taagttcaga cctggaccac ggtggtgtgc ggttcaaggc caggtggatg      240
226 aaaagacttt tcttactat gactgtggca gcaagacagt cacaccgctc agtcccctgg      300
228 ggaagaaact aaatgtcaca acggcctgga aagcacagaa ccagtagctg agagaggtgg      360
230 tggacatact tacagagcaa ctgcttgaca ttcagctgga gaattacata cccaaggaa      420
232 cctcaccct gcagccagg atgtcttgat agcagaaagc cgaaggacac ggcagtggat      480
234 cttggcagct cagtttcgat ggacagatct tctcctctt tgactcagaa aacagaatgt      540
236 ggacaacggt tcatcctgga gccagaaaga tgaaagaaaa gtgggagaat gacaaggata      600
238 tgaccatgtc ctccattac atctcaatgg gagactgcac aggatggctt gaggacttct      660
240 tgatgggcat ggacagcacc ctggagccaa gtgcaggagc accaccacc atgtcctcag      720
242 gcacagccca acccagggcc acggccacca cctcctcct ttgctgcctc ctcatcatgt      780
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246 tgcagcctcc tctcctcct cccctgcttc atcctacctg gctgctgaga agagtccttt      900
248 ggagtgcag ctaccaaata gcgaagcgcc ccttgtctgg tggacacgtg actcgctga      960
250 ctttacctat cattggagac gactcacact ccttacctg cctctctgcc ttgtatacaa      1020
252 taaataacgg cgcagccagg tattcggagc cactcaggct tccatatctt gatggttccc      1080
254 tgggcccagc tgtcttttct tccgtcaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1140
256 aaa                                                                                               1143
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261 <211> LENGTH: 939
263 <212> TYPE: DNA
265 <213> ORGANISM: Homo sapiens
269 <400> SEQUENCE: 4
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272 agctggtgca ggaccgggct ggccgacct cactctcttt gctatgacat caccgtcatc      120
274 cctaagttca gacctggacc accgtggtgt gcggttcaag gccaggtgga tgaaaagact      180
276 tttcttcaat atgactgtgg cagcaagaca gtcacaccgc tcagtccctt ggggaagaaa      240
278 ctaaatgtca caacggcctg gaaagcacag aaccagtagc tgagagaggt ggtggacata      300
280 cttacagagc aactgcttga cattcagctg gagaattaca taccgaagga acccctcacc      360
282 ctgcaggcca ggatgtcttg tgagcagaaa gccgaaggac acggcagtgg atcttggcag      420
284 ctcatgttct atggacagat ctctcctctc ttgactcag aaaacagaat gtggacaacg      480
286 gttcatcctg gagccagaaa gatgaaagaa aagtgggaga atgacaagga tatgaccatg      540
288 tccttccatt acatctcaat gggagactgc acaggatggc ttgaggactt cttgatgggc      600
290 atggacagca ccctggagcc aagtgcagga ggcacagtct gacccaaagc catggccacc      660
292 accctcagtc cctgcagcct cctcctcatc ctcccctgct tcatcctacc tggctgctga      720
294 ggagagtcc tggagtgac agctaccaa tagcgaagcg ccccttgtct ggtggacacg      780
296 tgactcgcgt gactttacct atcattggag acgactcaca ctcttacct tgcctcttg      840
298 ccttgatatac aataaataac ggcgcagcca ggtattcgga gccactacag gtctccatat      900
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303 <210> SEQ ID NO: 5
305 <211> LENGTH: 246

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309 <213> ORGANISM: Homo sapiens
313 <400> SEQUENCE: 5
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320 20 25 30
323 Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg Pro Gly Pro Arg
324 35 40 45
327 Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr Phe Leu His Tyr
328 50 55 60
331 Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser Pro Leu Gly Lys Lys
332 65 70 75 80
335 Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro Val Leu Arg Glu
336 85 90 95
339 Val Val Asp Ile Leu Thr Glu Gln Leu Arg Asp Ile Gln Leu Glu Asn
340 100 105 110
343 Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg Met Ser Cys Glu
344 115 120 125
347 Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln Phe Ser Phe Asp
348 130 135 140
351 Gly Gln Ile Phe Leu Leu Phe Asp Ser Glu Lys Arg Met Trp Thr Thr
352 145 150 155 160
355 Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys
356 165 170 175
359 Val Val Ala Met Ser Phe His Tyr Phe Ser Met Gly Asp Cys Ile Gly
360 180 185 190
363 Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser
364 195 200 205
367 Ala Gly Ala Pro Leu Ala Met Ser Ser Gly Thr Thr Gln Leu Arg Ala
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375 Phe Ile Leu Pro Gly Ile
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379 <210> SEQ ID NO: 6
381 <211> LENGTH: 263
383 <212> TYPE: PRT
385 <213> ORGANISM: Homo sapiens
389 <400> SEQUENCE: 6
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395 Leu Leu Leu Leu Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser
396 20 25 30
399 Leu Cys Phe Asn Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro
400 35 40 45
403 Trp Cys Glu Ala Gln Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr
404 50 55 60
407 Asn Ser Asp Asn Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys

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408 65          70          75          80
411 Val Asn Ala Thr Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu Gly Glu
412          85          90          95
415 Val Gly Arg Asp Leu Arg Met Leu Leu Cys Asp Ile Lys Pro Gln Ile
416          100          105          110
419 Lys Thr Ser Asp Pro Ser Thr Leu Gln Val Glu Met Phe Cys Gln His
420          115          120          125
423 Glu Ala Glu Arg Cys Thr Gly Ala Ser Trp Gln Phe Thr Ile Asn Gly
424          130          135          140
427 Glu Lys Ser Leu Leu Phe Asp Ala Met Asn Met Thr Trp Thr Val Ile
428 145          150          155          160
431 Asn His Glu Ala Ser Lys Ile Lys Glu Thr Trp Lys Lys Asp Arg Gly
432          165          170          175
435 Leu Glu Lys Tyr Phe Arg Lys Leu Ser Lys Gly Asp Cys Asp His Trp
436          180          185          190
439 Leu Arg Glu Phe Leu Gly His Trp Glu Ala Met Pro Glu Pro Thr Val
440          195          200          205
443 Ser Pro Val Asn Ala Ser Asp Ile His Trp Ser Ser Ser Ser Leu Pro
444          210          215          220
447 Asp Arg Trp Ile Ile Leu Gly Ala Phe Ile Leu Leu Val Leu Met Gly
448 225          230          235          240
451 Ile Val Leu Ile Cys Val Trp Trp Gln Asn Gly Glu Trp Gln Ala Gly
452          245          250          255
455 Leu Trp Pro Leu Arg Thr Ser
456          260
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461 <211> LENGTH: 244
463 <212> TYPE: PRT
465 <213> ORGANISM: Homo sapiens
469 <400> SEQUENCE: 7
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475 Pro Tyr Leu Leu Phe Asp Trp Ser Gly Thr Gly Arg Ala Asp Ala His
476          20          25          30
479 Ser Leu Trp Tyr Asn Phe Thr Ile Ile His Leu Pro Arg His Gly Gln
480          35          40          45
483 Gln Trp Cys Glu Val Gln Ser Gln Val Asp Gln Lys Asn Phe Leu Ser
484          50          55          60
487 Tyr Asp Cys Gly Ser Asp Lys Val Leu Ser Met Gly His Leu Glu Glu
488 65          70          75          80
491 Gln Leu Tyr Ala Thr Asp Ala Trp Gly Lys Gln Leu Glu Met Leu Arg
492          85          90          95
495 Glu Val Gly Gln Arg Leu Arg Leu Glu Leu Ala Asp Thr Glu Leu Glu
496          100          105          110
499 Asp Phe Thr Pro Ser Gly Pro Leu Thr Leu Gln Val Arg Met Ser Cys
500          115          120          125
503 Glu Cys Glu Ala Asp Gly Tyr Ile Arg Gly Ser Trp Gln Phe Ser Phe
504          130          135          140
507 Asp Gly Arg Lys Phe Leu Leu Phe Asp Ser Asn Asn Arg Lys Trp Thr

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VERIFICATION SUMMARY

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